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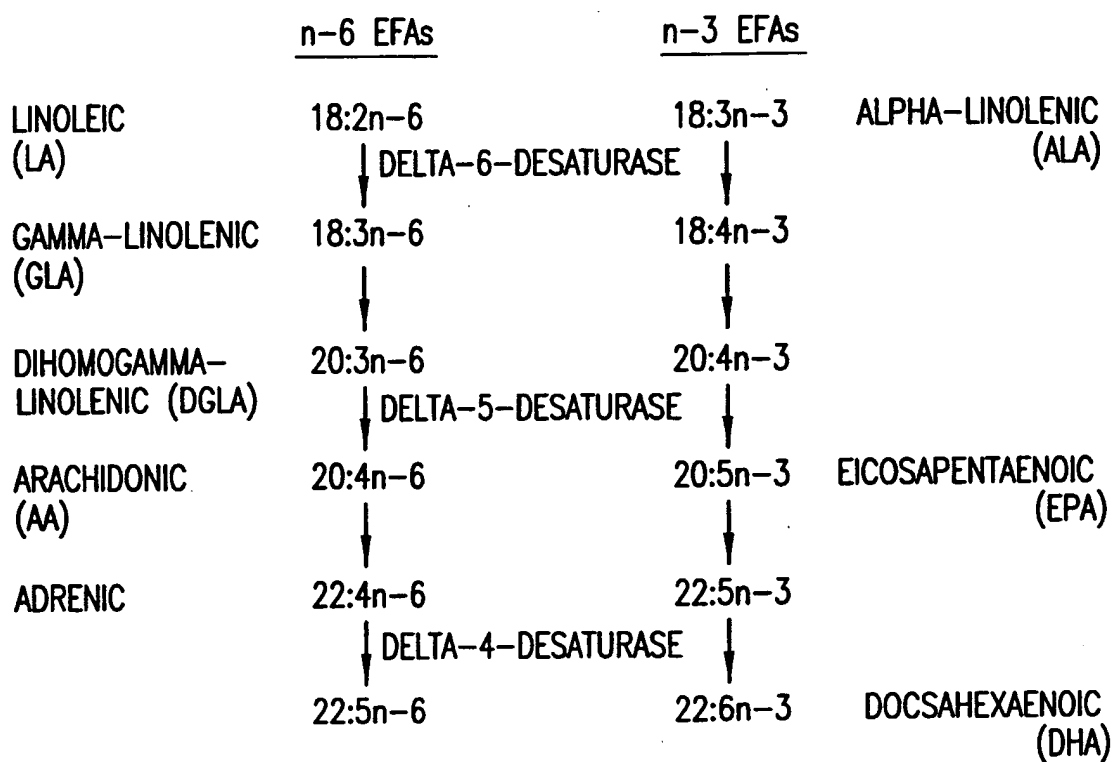


FIG.1

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0906088-074304

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251 cgcctggatt ggagcggacg cgggggtcag ccagccttgg gggccggggc
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401 ctcgtaaggc ggccgcggcg gcaggggcgg gccggagcag cgggcggcgg
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501 ACCTCGGCCA CCGCCTGGGA TCCCAGGAC TCGTGCCTGC AGCATGGGCG
551 GCGTCGGGGA GCCGGGACCG CGGGAGGGAC CCGCGCAGCC GGGGGCGCCG
601 CTGCCACCT TCTGCTGGGA GCAGATCCGC GCGCACGACC AGCCCGGCCA
651 CAAGTGGCTG GTCATCGAGC GCCGCGTCTA CGACATCAGC CGCTGGGCAC
701 AGCGGCACCC AGGGGGCAGC CGCCTCATCG GCCACCACGG CGCTGAGGAC
751 GCCACGgtaa ggaagccata aggaagccac ccaccggcgg gtggagcctg
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2201 cactcccggc ctgctctagt cttttgtaac ctaggaggaca gtatggatac
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2301 cccagactgg agtgcaatgg cgccatcttg gctcactgca acctccgcct
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2451 tttcaccatg ttggccaagc tgggtctcgaa ctocctgacct cgtgatccac
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FIG.2A

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 2701 caataatatc tgttttataaa acatctcagg ccgagcgctg tggctcacac
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FIG.2B

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 7951 ctgagagccc agcctgcttc ccagggaact gtcacagccc cacctgtccc

FIG.2C

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 10551 gagcccaggt gtgaagttca agcttacttt acttctgggc cacttctggtg
 10601 ctggtctctt tccctggccc ttatctttct cctggtctgt cttctcttct
 10651 caccctctt ctttactct tcttcttct cctgcatcgt actccacccc

FIG.2D

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 11501 ctgcagatgt ttgaccgtgt tcagagaggg gcccttggtc tgggtgaagt
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 13051 gcttctgacc ctgcctctct ccccagGCTC AGTCTGGTG TCTGCAGCAT
 13101 GACCTGGGCC ATGCCTCCAT CTTCAAGAAG TCCTGGTGGG ACCACGTGGC
 13151 CCAGAAGTTC GTGATGGGGC AGCTAAAGgt gaggggtggg tgggtggtca
 13201 gccagggtgct ggggtggcgt ggggtctgcc aagtgtgtgg gcacagtcgg
 13251 gggcacagcc tgccctgaga gccccctcct cctccacagG GCTTCTCCGC

FIG.2E

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0906088-07404

13301	CCACTGGTGG	AACTTCCGCC	ACTTCCAGCA	CCACGCCAAG	CCCAACATCT
13351	TCCACAAAGA	CCCAGACGTG	ACGGTGGCGC	CCGTCTTCCT	CCTGGGGGAG
13401	TCATCCGTCG	AGgtgggtgg	ggaggggacct	ggacaacctc	tggctggggc
13451	tgcagctgag	ggggagctaa	tgcactgggt	ccccactctg	cccctgacct
13501	agccccctgat	ctggcctcca	ctctggctgg	gccaagctct	gcccccggtg
13551	ctttccttcc	cacctcccaa	cctgctgggg	acgaccagcc	cgcttgctag
13601	aatctagagt	tgcctttgac	ccttggcccc	agccagcccc	gtgaccttgc
13651	ccgggagaag	gaggtggcct	ggagagctgc	tgtctccagc	cgccgctgtg
13701	ctccacagTA	TGGCAAGAAG	AAACGCAGAT	ACCTACCCTA	CAACCAGCAG
13751	CACCTGTACT	TCTTCCTGAg	tgagtgtcca	tctgtccttc	tggggtgggg
13801	gagtgcctgg	gcctgcactg	tctccctgc	tgtcctggac	cactcccagc
13851	cacttctctg	ggcggggcac	gtctgtcagg	tctccctggt	catggcatcc
13901	tcccagcctc	tgcagtctgt	acacactctc	ccagcagcat	gcctttgccc
13951	cagctgtctc	ccgtgcctgg	gacaccttgc	agccacgggc	catcacagcc
14001	ctgctgggag	cttccccaa	ccccacgtag	aatttcttct	tgcctcact
14051	agagtgggtc	ggagccctag	agtctttggg	cagttgttgg	ggcggacaga
14101	gtgaggactc	aagtctggcc	ctgacttgcg	gtgaagggtg	gtgggaggtg
14151	gtggggtaag	ggcagcctgg	ggaggcttgg	acacagaatt	gggggtgata
14201	tggggtcatt	cagctggatg	tgaccagcac	caacgtccca	ggggcattcc
14251	tggagtaaca	gagccccca	ctctggcgcc	cactcacctt	ggcagcccag
14301	ccccactcct	gaacactctc	atgccccctc	ttgcagTCGG	CCCGCCGCTG
14351	CTCACCTGG	TGAACCTTGA	AGTGGAAAAT	CTGGCGTACA	TGCTGGTGTG
14401	CATGCAGTGG	GCGgtgagtg	gggttgccca	ggacccccgg	catacggctg
14451	ccgtggcagg	aggtggtgcc	tcgggggaca	gtacctgccc	atgaaggcaa
14501	acagggtgca	catgtgcgtg	caacagtgtg	gtcacatgt	atgcgtgcaa
14551	cagtgtggct	cacatgtgtg	cgcgagcag	gagagcgagt	gtgcccgtga
14601	ctgtacgtgt	ggtggggggg	ggttgaggaa	cagggggggg	gtgggtctct
14651	ctcggtgagg	gtgtcttccc	aggaggagtt	gctgggccga	ctctgccagg
14701	catctgtgtc	cctggcaggg	tcttccccaa	cacaccttgc	atgacacctt
14751	cgtcactaaa	atcagcctcg	tgagctggca	gggcaaggac	ctgttctctt
14801	tactcagctg	agaaaaccag	agagggtggt	ggcctgtcct	gggctctgag
14851	gcaaatcagg	cagaagggtt	ggatgcctga	ggtcctctct	ccacccacca
14901	ggcctccaga	cctccgggca	cctggagacc	tctcggtatc	gcctctgccc
14951	tctctgcag	GATTTGCTCT	GGGCCGCCAG	CTTCTATGCC	CGCTTCTTCT
15001	TATCTACCT	CCCCTTCTAC	GGCGTCCCTG	GGGTGCTGCT	CTTCTTTGTT
15051	GCTGTCAGgt	atggcaggga	gtggcgaggt	cacacacagg	cgacagggtga
15101	ccccactgc	agccccccac	cagagcttcc	cttttcccgt	ctgcagaatg
15151	gggccagtgg	tactgcctcc	ctggcttgct	ggtggaatca	cataaacaca
15201	agcgtggcag	gagcccaggg	tgggtgggtt	tagggagcgt	ggcctggctt
15251	gtaagtggcc	cggtgggtgt	cggagctgct	ctggactcag	cctcacagtg
15301	gacactgctc	cattcagatt	ctttaaacac	tggcaagggg	gcgatggcca
15351	caatcctatt	gtacagataa	ggaagtcaag	gccacttggg	gacagctgct
15401	ctccagcctc	cactcagggt	gcctaagtgg	tgagctggac	ctagggcagt
15451	gcccagacct	ccccacagGG	TCCTGGAAAG	CCACTGGTTC	GTGTGGATCA
15501	CACAGATGAA	CCACATCCCC	AAGGAGATCG	GCCACGAGAA	GCACCGGGAC
15551	TGGGTCAGCT	CTCAGgtggg	cagcaggggt	ggggcccatc	ctgggtgggg
15601	tgggggggtcc	cagctaggag	ccagatggca	aagcagggat	gaggccctga
15651	cggggctgcc	aggtggggga	tgggtccgtg	gggtcagggg	tctgcaacgg
15701	cctcctcaca	tgtgccccgc	cggcttccgg	cagCTGGCAG	CCACCTGCAA
15751	CGTGGAGCCC	TCACTTTTCA	CCAAGTGGTT	CAGCGGGCAC	CTCAACTTCC
15801	AGATCGAGCA	CCAgtagagt	tgggtgctgg	gggacagtgg	gaggtgggga
15851	gggggtcctg	ggaggggatc	ctgggagggg	acccgtgggt	ggggcctctc

FIG.2F

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15901 tctggaatct cccacttcag gtgccagcat acgctcccca cccccagCCT
 15951 CTTCCCCAGG ATGCCGAGAC ACAACTACAG CCGGGTGGCC CCGCTGGTCA
 16001 AGTCGCTGTG TGCCAAGCAC GGCCTCAGCT ACGAAGTGAA GCCCTTCCTC
 16051 ACCGCGCTGG TGGACATCGT CAGgtgaggc tgcagcccg cccctctgtt
 16101 ctggtggctt ccccagggcc tatgcctacc cttgtccagg tcagcctcat
 16151 gctgagcccc cagggtcctt gaggctttct gtccacgtcc catgcccttc
 16201 ctcccttccc cagccttcac gcacacagtg agaattttctg gagcacctac
 16251 tgcagactca caaacagcag tgcctgcggt gagcaggctc atgcaaacct
 16301 acccccaaag gctgaggga aaaagctaac agatccagtt tctcagaagg
 16351 aaacacttaa cagggactca taaacagaag ccatgtctca gggccgggtg
 16401 cgggtggctca cgcctgtaat tccagcactt ggggaggctg aggtgggagg
 16451 atcacttgag gtcaggagt cgagaccagc ctggccaaca tggtgaaacc
 16501 ccgtctctac taaaaaaaaa aaaaaaaaaa aaaacaaaac aaaaattagc
 16551 tgggtgtggt ggcagggtgcc cataatccca gctacttggg aggtgaggg
 16601 aggagaatca cttgaactcg caggggcaga ggttgcagtg agctgagatt
 16651 gtgcctttgc agtccagcct gggcaacaga gcaagactct ctcaaaaaca
 16701 aacaaaaaaa ccatgtctca ggcagccaag agttgggaca tccctcaca
 16751 cgccctctag aaagaaccct ctatatagca agcttttagg gtgaacccca
 16801 tgcagggtgt tcttatgaac ctggtgacca ctggagggtta gataagcgctc
 16851 tacaagagga ggttatctat gccatgagct tggcattcag ggtcaagcat
 16901 cggtcctcag acagttttgc ttgaagatgg cattgccctt gtagcaatgc
 16951 aggtctctaga gagcttcctg ccctcttgga gctgatgttc cttccagcaa
 17001 aggaaacagc aagcaattaa aataacaaat aagtacatta cagaagatgg
 17051 gcaaaagaac aatgaaaagc ccctcagggt ggggacaggg gaggggaggg
 17101 gggcgggccag gcagggggcg cagtttctaa ataggtggtta ggggtgggag
 17151 tattgacagg ctgacgtgtg agcagggaca gggagggagg gagaggtctc
 17201 gccacagga catctggcaa agagcggtca ggcagagggc acttgaccct
 17251 gaatgccaag ctcatggcat agatagccga ggcaggcatg caggcactca
 17301 gagaagggac acgcccggct tgcactttgg aaagctgccc ctactgggaa
 17351 tgactggcgg gcaggagtcg aagtggaaaa ggagagcaga ggacactgca
 17401 gccatccagg cgaggggtga tggggctcag cccttgtggt caccttggag
 17451 gtggggaaca gagggccagat tccaggctct atacctctgc gcctttgtac
 17501 acgctgttcc ccttacttgg ttgcccttcc ttcctgtgct ggtgttcaga
 17551 tgcccacttc tcttcatga tctctcccag cctgatgctc tgagcccctg
 17601 ccatttgga cagcccttta gagcgcttg cacagggtt cctagcagat
 17651 tggtgacatt tctggctcca ctgccaata tcaggcccaa gatcggtgg
 17701 gcaggttcca cgtcctctct gtcttgggt tgcagcgccc agcaggaggc
 17751 agcaatggag aactgggtgc aggagggaca ggccaccca ggctcatgcc
 17801 tggacttggc cttggctgcc ctccagctcc cctaccgac acccgtcacc
 17851 ccggtctaga ttccattcca gagaatgagc attcagctgt tctcccaacc
 17901 caccctccag cccgcatcgc tgctgcccc cagggaaggg aaccacagg
 17951 gaatgggat ctccgctcac acttaccatg ggggatacag ggtgttagg
 18001 atcttgcaac tgagctccta acaccaccc ccatgccac cccacctcc
 18051 cagGTCCCTG AAGAAGTCTG GTGACATCTG GCTGGACGCC TACCTCCATC
 18101 AGTGAAGGCA ACACCCAGGC GGCAGAGAA GGGCTCAGGG CACCAGCAAC
 18151 CAAGCCAGCC CCCGGCGGGA TCGATACCC CACCCCTCCA CTGGCCAGCC
 18201 TGGGGGTGCC CTGCCGTGCC TCCTGGTACT GTGTCTTCC CCTCGGCCCC
 18251 CTCACATGTG TATTCAGCAG CCCTATGGCC TTGGCTCTGG GCCTGATGGG
 18301 ACAGGGGTAG AGGGAAGGTG AGCATAGCAC ATTTTCTAG AGCGAGAATT
 18351 GGGGGAAAGC TGTTATTTTT ATATTAAAT ACATTCAGAT GTATTATGGA
 18401 GT

FIG.2G

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1	CTTCGCTTCCTCGGGTCTTGCTCGGACCTCGGCCACCGCCTGGGATCC	50
51	CCAGGACTCGTGCGTGACGATGGGCGGCGTCGGGGAGCCGGGACCGCGG	100
1	M G G V G E P G P R	10
101	GAGGGACCCGCGCAGCCGGGGGACCGCTGCCACCTTCTGCTGGGAGCA	150
11	E G P A Q P G A P L P T F C W E Q	27
151	GATCCGCGCGCACGACCAGCCCGGCGACAAGTGGCTGGTCATCGAGCGCC	200
28	I R A H D Q P G D K W L V I E R R	44
201	GCGTCTACGACATCAGCCGCTGGGCACAGCGGCACCCAGGGGGCAGCCGC	250
45	V Y D I S R W A Q R H P G G S R	60
251	CTCATCGGCCACCACGGCGCTGAGGACGCCACGGATGCCTTCCGTGCCTT	300
61	L I G H H G A E D A T D A F R A F	77
301	CCATCAAGATCTCAATTTTGTGCGCAAGTTCCTACAGCCCCTGTTGATTG	350
78	H Q D L N F V R K F L Q P L L I G	94
351	GAGAGCTGGCTCCGGAAGAAGCCAGCCAGGATGGACCCCTGAATGCGCAG	400
95	E L A P E E P S Q D G P L N A Q	110
401	CTGGTCGAGGACTTCCGAGCCCTGCACCAGGCAGCCGAGGACATGAAGCT	450
111	L V E D F R A L H Q A A E D M K L	127
451	GTTTGATGCCAGTCCCACCTTCTTTGCTTTCCTACTGGGCCACATCCTGG	500
128	F D A S P T F F A F L L G H I L A	144
501	CCATGGAGGTGCTGGCCTGGCTCCTTATCTACCTCCTGGGTCTGGCTGG	550
145	M E V L A W L L I Y L L G P G W	160
551	GTGCCCAGTGCCCTGGCCGCTTCATCCTGGCCATCTCTCAGGCTCAGTC	600
161	V P S A L A A F I L A I S Q A Q S	177
601	CTGGTGTCTGCAGCATGACCTGGGCCATGCCTCCATCTTCAAGAAGTCCT	650
178	W C L Q H D L G H A S I F K K S W	194
651	GGTGGAACCACGTGGCCCCAGAAGTTCGTGATGGGGCAGCTAAAGGGCTTC	700
195	W N H V A Q K F V M G Q L K G F	210

FIG.3A

09806088-071304

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701 TCCGCCCACTGGTGGAACTTCCGCCACTTCCAGCACCACGCCAAGCCCAA 750
211 S A H W W N F R H F Q H H A K P N 227

751 CATCTTCCACAAAGACCCAGACGTGACGGTGGCGCCCGTCTTCCTCCTGG 800
228 I F H K D P D V T V A P V F L L G 244

801 GGGAGTCATCCGTCGAGTATGGCAAGAAGAAACGCAGATACCTACCCTAC 850
245 E S S V E Y G K K K R R Y L P Y 260

851 AACCAGCAGCACCTGTACTTCTTCTGATCGGCCCGCCGCTGCTCACCT 900
261 N Q Q H L Y F F L I G P P L L T L 277

901 GGTGAAC TTTGAAGTGGAAAATCTGGCGTACATGCTGGTGTGCATGCAGT 950
278 V N F E V E N L A Y M L V C M Q W 294

951 GGGCGGATTTGCTCTGGGCCGCCAGCTTCTATGCCCCGCTTCTTCTTATCC 1000
295 A D L L W A A S F Y A R F F L S 310

1001 TACCTCCCCTTCTACGGCGTCCCTGGGGTGCTGCTCTTCTTTGTTGCTGT 1050
311 Y L P F Y G V P G V L L F F V A V 327

1051 CAGGGTCCTGGAAAGCCACTGGTTCGTGTGGATCACACAGATGAACCACA 1100
328 R V L E S H W F V W I T Q M N H I 344

1101 TCCCCAAGGAGATCGGCCACGAGAAGCACCGGGACTGGGTACAGCTCTCAG 1150
345 P K E I G H E K H R D W V S S Q 360

1151 CTGGCAGCCACCTGCAACGTGGAGCCCTCACTTTTCACCAACTGGTTCAG 1200
361 L A A T C N V E P S L F T N W F S 377

1201 CGGGCACCTCAACTTCCAGATCGAGCACCACCTCTTCCCCAGGATGCCGA 1250
378 G H L N F Q I E H H L F P R M P R 394

1251 GACACAAC TACAGCCGGGTGGCCCCGCTGGTCAAGTCGCTGTGTGCCAAG 1300
395 H N Y S R V A P L V K S L C A K 410

1301 CACGGCCTCAGCTACGAAGTGAAGCCCTTCTCACC GCGCTGGTGGACAT 1350
411 H G L S Y E V K P F L T A L V D I 427

1351 CGTCAGGTCCCTGAAGAAGTCTGGTGACATCTGGCTGGACGCCTACCTCC 1400
428 V R S L K K S G D I W L D A Y L H 444

FIG.3B



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1401	ATCAGTGAAGGCAACACCCAGGCGGGCAGAGAAGGGCTCAGGGCACCAGC	1450
445	Q	445
1451	AACCAAGCCAGCCCCCGGCGGGATCGATACCCCCACCCTCCACTGGCCA	1500
1501	GCCTGGGGGTGCACTGCCTGCCCTCCTGGTACTGTTGTCTTCCCCTCGGC	1550
1551	CCCCTCACATGTGTATTCAGCAGCCCTATGGCCTTGGCTCTGGGCCTGAT	1600
1601	GGGACAGGGGTAGAGGGAAGGTGAGCATAGCACATTTTCCTAGAGCGAGA	1650
1651	ATTGGGGGAAAGCTGTTATTTTTATATTAATAACATTCAGATGTAAAAA	1700

FIG.3C

09806088-071301

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1 GTACAGCGGCAATGGGCGGTGTCGGGGAGCCCGGAGGGGGACTCGGGCCG 50
1 M G G V G E P G G G L G P 13

51 CGGGAGGGGGCCCGCACCGCTGGGGGCGCCCCTACCCATCTTCCGCTGGGA 100
14 R E G P A P L G A P L P I F R W E 30

101 GCAGATCCGCCAGCATGACCTACCAGGCGACAAGTGGCTGGTCATCGAGC 150
31 Q I R Q H D L P G D K W L V I E R 47

151 GCCGTGTCTACGACATCAGCCGCTGGGCACAGCGGCACCCAGGGGGTAGC 200
48 R V Y D I S R W A Q R H P G G S 63

201 CGCATCATCGGCCACCACGG 220
64 R I I G H H 69

FIG.4

T02120-88090880

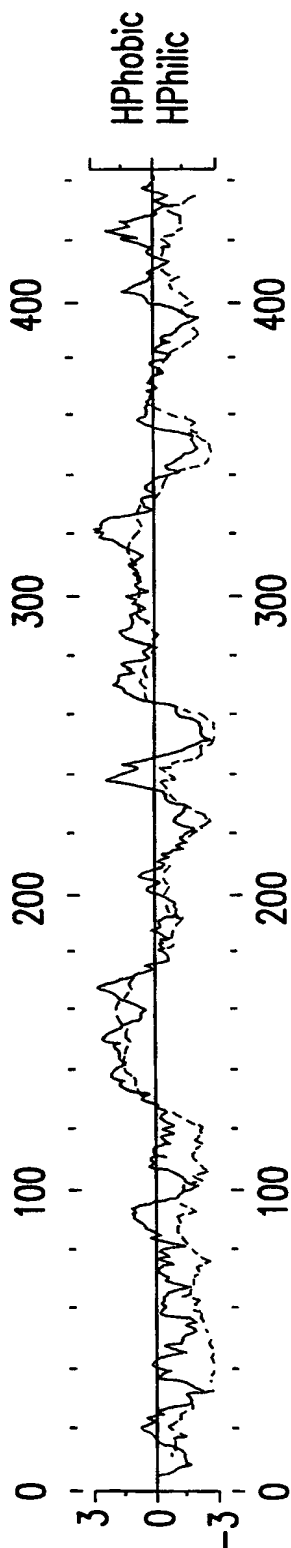
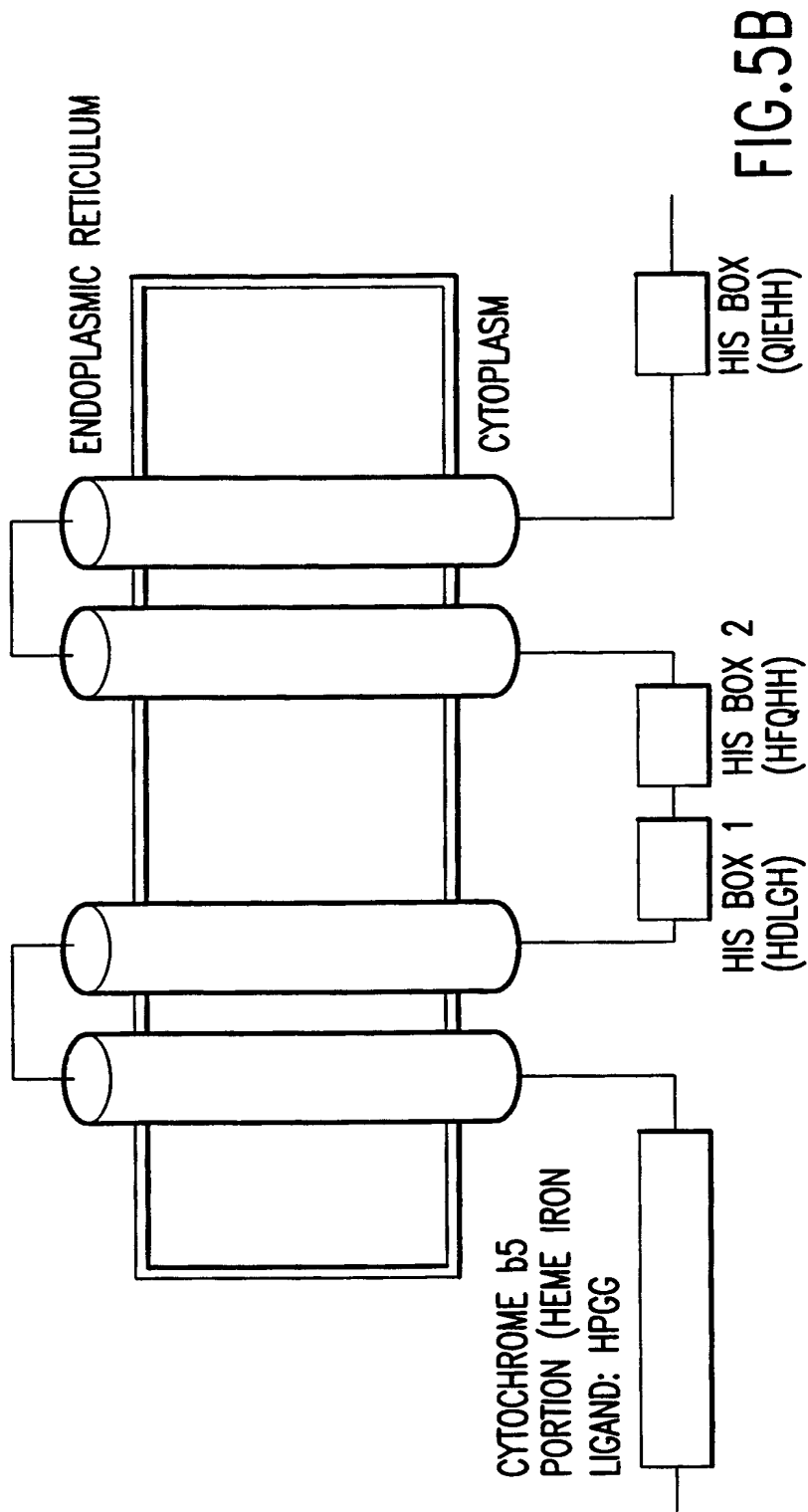


FIG.5A



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PROFILESCAN of : CYB5rp_correct_protein check: 5714 from: 1 to: 445

GETSEQ from bmd, December 2, 1997 14:20.

Compare to profile library: GenRunData:profilesca.n.fil

Profile: profiledir:cytochrome_b5.prf

Gap weight: 4.50 Gap Length weight: 0.05

Ave match: 0.27 Ave mismatch : -0.21

(Peptide) PROFILEMAKE v4.40 of: 0191.Msf2{*} Length: 48

Sequences: 24 MaxScore: 27.58 December 2, 1992 00:07

This profile is derived from PROSITE release 10.0 and has been tested by a database search against SWISS-PROT release 26.0. A comparison of the SWISS-PROT annotation and the results of the database search follows. For further information about this motif, consult the . . .

Profile: profiledir:cytochrome_b5.prf alignment: 1

Quality: 20.77 Gaps: 0

Ratio: 0.43 Length: 48

Normalized quality: 2.91

S 31 HDQPGDKWLVIERRVYDISRWAQRHPGGSRLIGHGAEDATDAFRAFH 78

|: .: |||. .|||::| . |||. | .||.:||. |::|

P 1 HNDGEETWLVNGQVYDITKFLLEHPGGPDVIMEAAGTDATEEFEAIH 48

*Cytochrome b5 family, heme-binding domain signature *

FIG.6

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pir:s68358 hypothetical protein - common sunflower
Length = 458

Score = 169 (79.4 bits), Expect = $2.8e-42$, Sum P(4) = $2.8e-42$
Identities = 31/85 (36%), Positives = 49/85 (57%)

His box 3

Query: 348 IGHEKHRDWSSQLAATCNVEPSLFTNWFSGHLNFQIEHHLFPRMPRHNYSRVAPLVKSL 407
+G K +W Q T ++ S + +WF G L FQ+EHHLFPR+PR + ++P+ + L
Sbjct: 348 VGPPKGDNWF EKQTRGTIDACSSWMDWFFGGLQFQLEHHLFPRLPCHLRSISPICREL 407

Query: 408 CAKHGLSYEVKPF LTALVDIVRSLK 432
C K+ L Y F A V +++L+
Sbjct: 408 CKKYNLPYVSLSFYDANVTTLKTLR 432

Score = 133 (62.5 bits), Expect = $2.8e-42$, Sum P(4) = $2.8e-42$
Identities = 21/53 (39%), Positives = 35/53 (66%)

HPGG motif

Query: 26 EQIRAHDPQGDKWLVIERRVYDISRWAQRHPGGSRLLIGHHGAEDATDAFAFH 78
++++ H+ P D W+ I +VY+++ WA+ HPGG + + +D TDAF AFH
Sbjct: 22 KELKKHNNPNDLWISILGKVYNVTEWAKEHPGGDAPLINLAGQDVTDAF IAFH 74

Score = 118 (55.5 bits), Expect = $2.8e-42$, Sum P(4) = $2.8e-42$
Identities = 25/76 (32%), Positives = 34/76 (44%)

His box 1

His box 2


Query: 165 LAAFILAISSQAQSWCLOHDLGHASIFKKSWMNHVAQKFVMGQLKGFSAHWWNFRHFQHEA 224
L+ IL ++ Q L HD GH + WN A F+ + G S WW + H HH
Sbjct: 152 LSGAILGLAWMQIAYLGHDAAGHYQMMATRGWNKFAGIFIGNCITGISIAWWKWNTHNAHI 211

Query: 225 KPNIFHKDPDVTVPV 240
N DPD+ P+
Sbjct: 212 ACNSLDYDPDLQHLPM 227

Score = 34 (16.0 bits), Expect = $2.8e-42$, Sum P(4) = $2.8e-42$
Identities = 7/14 (50%), Positives = 9/14 (64%)

FIG. 7A

0906088:01301

 gp:bou79010 1 PID:g2062403 *Borago officinalis* delta 6 desaturase mRNA,
 complete cds. (gb:U79010) (NID:2062402)
 Length = 448

Score = 179 (84.1 bits), Expect = 2.3e-42, Sum P(3) = 2.3e-42
Identities = 34/87 (39%), Positives = 48/87 (55%)

Query: 348 IGHEKHRDWSSQLAATCNVEPSLFTNWFSGHLNFQIEHHLFPRMPRHNYSRVAPLVKSL 407
+G K +W Q T ++ + +WF G L FQIEHHLFP+MPR N +++P V L
Sbjct: 338 VGKPKGNNWFEKQTDGTLDISCPPWMDWFHGGLOFQIEHHLFPKMPRCNLRKISPYVIEL 397

Query: 408 CAKHGLSYEVKPF LTALVDIVRS LKKS 434
C K H L Y F A +R+L+ +
Sbjct: 398 CKKHNL PYNYASF SKANEMTLRLTRNT 424

Score = 144 (67.7 bits), Expect = 2.3e-42, Sum P(3) = 2.3e-42
Identities = 23/53 (43%), Positives = 36/53 (67%)

Query: 26 EQIRAHDPGDKWLVIERRVYDISRWAQRHPGGSRLIGHGAEDATDAFRAFH 78
 +++ HD+PGD W+ I+ + YD+S W + HPGGS + ++ TDAF AFH
 Sbjct: 12 DELKNHDKPGDLWISIQGKAYDVSDDWKDHPGGSFPLKSLAQEVTDAFVAFH 64

Score = 105 (49.3 bits), Expect = 2.3e-42, Sum P(3) = 2.3e-42
Identities = 22/68 (32%), Positives = 28/68 (41%)

Query: 176 QSWCLOHDLGHASIFKKSWNNHVAQKFMGQLKGFSAHWWNFRHFQHHAKPNIFHKDPDV 235
 QS + HD GH + S N F L G S WW + H HH N DPD+

Sbjct: 153 QSGWIGHDAGHYMVVSDSRLNKFMGIFAANCLSGISIGWKKWNHNAHHIACNSLEYDPDL 212

Query: 236 TVAPVFLL 243
p ++
Subject: 213 QVIPFLVV 220

FIG. 7B

FIG.8

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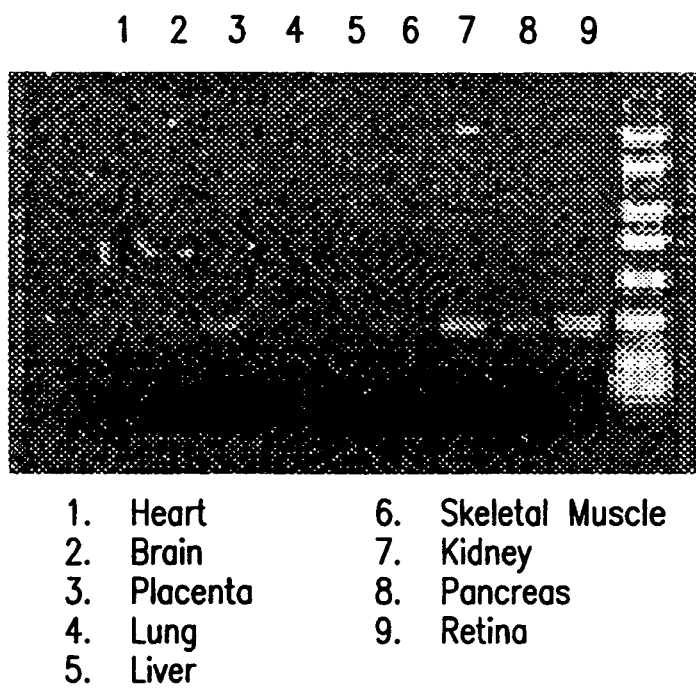


FIG.9A

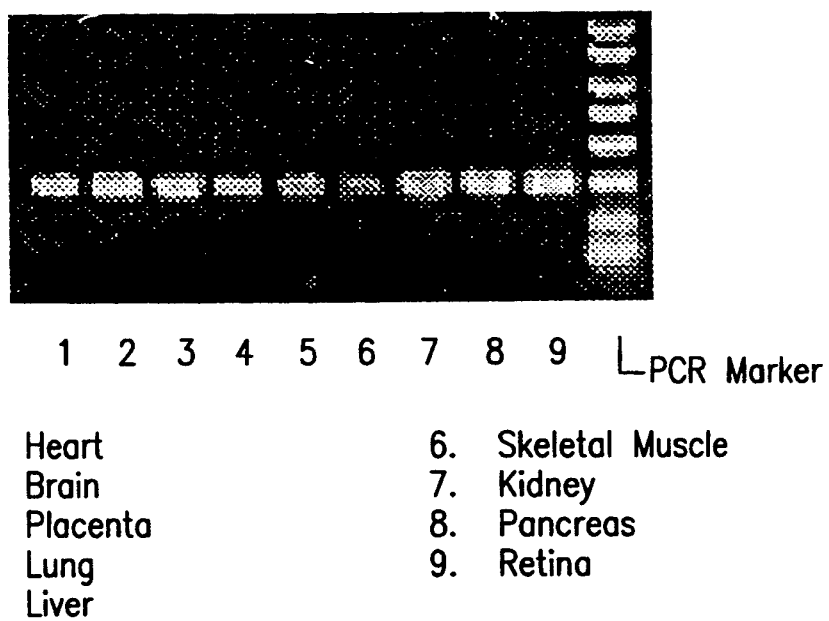
[illegible]

FIG. 9B